SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT: SHEPARD, H. M.
                 KAN, NANCY

    (ii) TITLE OF INVENTION: GENE THERAPY BY RETROVIRAL VECTOR WITH
           TUMOR SUPPRESSIVE GENE

    (iii) NUMBER OF SEQUENCES: 2

    (iv) CORRESPONDENCE ADDRESS:
        (A) ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW LLP
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        (C) CITY: SAN FRANCISCO
        (D) STATE: CA
        (E) COUNTRY: U.S.A.
        (F) ZIP: 94111-3834

    (v) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: Floppy disk
        (B) COMPUTER: IBM PC compatible
        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
        (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

    (vi) CURRENT APPLICATION DATA:
        (A) APPLICATION NUMBER: US 08/403,797
        (B) FILING DATE: 04-DEC-1995
        (C) CLASSIFICATION:

    (vii) PRIOR APPLICATION DATA:
        (A) APPLICATION NUMBER: PCT/US95/08844
        (B) FILING DATE: 17-SEP-1993

    (viii) ATTORNEY/AGENT INFORMATION:
        (A) NAME: FITTS, RENEE A
        (B) REGISTRATION NUMBER: 35,136
        (C) REFERENCE/DOCKET NUMBER: 16930-000600

    (ix) TELECOMMUNICATION INFORMATION:
        (A) TELEPHONE: (415) 326-2400
        (B) TELEFAX: (415) 576-0300

(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 7 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: not relevant
        (D) TOPOLOGY: not relevant

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

    Ser His Arg Pro Gly Ser Arg
    1   5

(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 428 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: not relevant
        (D) TOPOLOGY: not relevant

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Leu Leu Gly Ser Gly Asp Thr Leu Arg Ser Gly Trp Glu Arg Ala Phe
1               5               10              15

His Asp Gly Asp Thr Leu Pro Trp Ile Gly Ser Gln Thr Ala Phe Arg
            20              25              30

Val Thr Ala Met Glu Glu Pro Gln Ser Asp Pro Ser Val Glu Pro Pro
        35              40              45

Leu Ser Gln Glu Thr Phe Ser Asp Leu Trp Lys Leu Leu Pro Glu Asn
    50              55              60

Asn Val Leu Ser Pro Leu Pro Ser Gln Ala Met Asp Asp Leu Met Leu
65              70              75              80

Ser Pro Asp Asp Ile Glu Gln Trp Phe Thr Glu Asp Pro Gly Pro Asp
            85              90              95

Glu Ala Pro Arg Met Pro Glu Ala Ala Pro Pro Val Ala Pro Ala Pro
            100             105             110

Ala Ala Pro Thr Pro Ala Ala Pro Ala Pro Ala Pro Ser Trp Pro Leu
        115             120             125

Ser Ser Ser Val Pro Ser Gln Lys Thr Tyr Gln Gly Ser Tyr Gly Phe
    130             135             140

Arg Leu Gly Phe Leu His Ser Gly Thr Ala Lys Ser Val Thr Cys Thr
145             150             155             160

Tyr Ser Pro Ala Leu Asn Lys Met Phe Cys Gln Leu Ala Lys Thr Cys
            165             170             175

Pro Val Gln Leu Trp Val Asp Ser Thr Pro Pro Pro Gly Thr Arg Val
            180             185             190

Arg Ala Met Ala Ile Tyr Lys Gln Ser Gln His Met Thr Glu Val Val
            195             200             205

Arg Arg Cys Pro His His Glu Arg Cys Ser Asp Ser Asp Gly Leu Ala
    210             215             220

Pro Pro Gln His Leu Ile Arg Val Glu Gly Asn Leu Arg Val Glu Tyr
225             230             235             240

Leu Asp Asp Arg Asn Thr Phe Arg His Ser Val Val Val Pro Tyr Glu
            245             250             255

Pro Pro Glu Val Gly Ser Asp Cys Thr Thr Ile His Tyr Asn Tyr Met
            260             265             270
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 Cys Asn Ser Ser Cys Met Gly Gly Met Asn Arg Arg Pro Ile Leu Thr
         275             280             285

 Ile Ile Thr Leu Glu Asp Ser Ser Gly Asn Leu Leu Gly Arg Asn Ser
         290             295             300

 Phe Glu Val Arg Val Cys Ala Cys Pro Gly Arg Asp Arg Arg Thr Glu
 305             310             315             320

 Glu Glu Asn Leu Arg Lys Lys Gly Glu Pro His His Glu Leu Pro Pro
             325             330             335

 Gly Ser Thr Lys Arg Ala Leu Pro Asn Asn Thr Ser Ser Ser Pro Gln
             340             345             350

 Pro Lys Lys Lys Pro Leu Asp Gly Glu Tyr Phe Thr Leu Gln Ile Arg
         355             360             365

 Gly Arg Glu Arg Phe Glu Met Phe Arg Glu Leu Asn Glu Ala Leu Glu
         370             375             380

 Leu Lys Asp Ala Gln Ala Gly Lys Glu Pro Gly Gly Ser Arg Ala His
 385             390             395             400

 Ser Ser His Leu Lys Ser Lys Lys Gly Gln Ser Thr Ser Arg His Lys
             405             410             415

 Lys Leu Met Phe Lys Thr Glu Gly Pro Asp Ser Asp
             420             425
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